

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 1, 2002, 05:37:35 ; Search time 5265 Seconds

(without alignments)
16995.607 Million cell updates/sec

Title: US-09-730-559B-1

Perfect score: 4276

Sequence: 1 ttctaccgcttttccctgc.....atcagaaaaaaaaaaaaaa 4276

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_ph:*
7: gb_pl:*
8: gb_pr:*
9: gb_ro:*
10: gb_ro:*
11: gb_ro:*
12: gb_ro:*
13: gb_ro:*
14: gb_ro:*
15: gb_ro:*
16: gb_ro:*
17: gb_ro:*
18: gb_ro:*
19: gb_ro:*
20: gb_ro:*
21: gb_ro:*
22: gb_ro:*
23: gb_ro:*
24: gb_ro:*
25: gb_ro:*
26: gb_ro:*
27: gb_ro:*
28: gb_ro:*
29: gb_ro:*
30: gb_ro:*
31: gb_ro:*
32: gb_ro:*
33: gb_ro:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB ID	Description
------------	-------	-------	--------	-------	-------------

1	3690.4	86.3	167659	2	AC023404	AC023404 Homo sapi
2	3690.4	86.3	175793	2	AC083300	AC083300 Homo sapi
3	3690.4	86.3	160130	2	AC093275	AC093275 Homo sapi
4	2480.4	56.0	157340	2	AC027609	AC027609 Homo sapi
5	912.6	21.3	6380	2	AB051460	AB051460 Homo sapi
6	467.4	10.9	212601	2	AL662793	AL662793 Mus muscu
7	467.4	10.9	249657	2	AL669946	AL669946 Mus muscu
8	430	10.1	5715	2	AB023157	AB023157 Homo sapi
9	364.6	9.3	71171	2	AC100917	AC100917 Mus muscu
10	304.6	7.1	13054	2	AY052043	AY052043 Drosophila
11	304.6	7.1	103054	2	AC014803	AC014803 Drosophila
12	304.6	7.1	181720	2	AC010114	AC010114 Drosophila
13	304.6	7.1	287018	2	AE003553	AE003553 Drosophila
14	240.6	5.6	205307	2	AC009968	AC009968 Homo sapi
15	238	5.6	97037	2	AC004973	AC004973 Homo sapi
16	238	5.6	126000	2	AP000074	AP000074 Homo sapi
17	238	5.6	135038	2	HEK293T703	HEK293T703 Homo sapi
18	238	5.6	180132	2	AF002354	AF002354 Homo sapi
19	237	5.6	113687	2	AC069281	AC069281 Homo sapi
20	237	5.3	179245	2	AC069281	AC069281 Homo sapi
21	231.4	5.4	203959	2	AC064827	AC064827 Homo sapi
22	230.4	5.4	133475	2	AC006254	AC006254 Homo sapi
23	230.2	5.4	183300	2	AC091489	AC091489 Homo sapi
24	230.2	5.4	181532	2	CNS01DM2	AL1136298 Human chr
25	230.2	5.4	187696	2	AC008785	AC008785 Homo sapi
26	229.4	5.4	155691	2	AC016868	AC016868 Homo sapi
27	229.4	5.4	214872	2	AC009720	AC009720 Homo sapi
28	228.6	5.3	166889	2	AC027008	AC027008 Homo sapi
29	228.6	5.3	167412	2	AL356352	AL356352 Homo sapi
30	228.6	5.3	169663	2	AL158307	AL158307 Homo sapi
31	228.6	5.3	241288	2	AC011499	AC011499 Homo sapi
32	228.4	5.3	147224	2	AP003779	AP003779 Homo sapi
33	228.4	5.3	161252	2	AC087464	AC087464 Homo sapi
34	228.4	5.3	177998	2	AL353562	AL353562 Homo sapi
35	228.4	5.3	112425	2	AC092573	AC092573 Homo sapi
36	228.4	5.3	208729	2	AC011667	AC011667 Homo sapi
37	228.4	5.3	125177	2	AC012052	AC012052 Homo sapi
38	228.4	5.3	162589	2	AC011667	AC011667 Homo sapi
39	228	5.3	180465	2	AC022076	AC022076 Homo sapi
40	228	5.3	196769	2	AC074011	AC074011 Homo sapi
41	228	5.3	207922	2	AC092164	AC092164 Homo sapi
42	227.8	5.3	84388	2	AL589984	AL589984 Human DNA
43	227.4	5.3	159634	2	AC010193	AC010193 Homo sapi
44	227.2	5.3	163891	2	AC092647	AC092647 Homo sapi
45	227	5.3	172789	2	AC104020	AC104020 Homo sapi

ALIGNMENTS

RESULT	1	AC023404	167659 bp	DNA	linear	HTG 01-MAR-2000
LOCUS	AC023404	Homo sapiens clone RP11-619L12, WORKING DRAFT SEQUENCE, 10				
DEFINITION	AC023404	unoriented pieces.				
ACCESSION	AC023404.2	GI:7139760				
VERSION	AC023404.2	GI:7139760				
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 167659)					
AUTHORS	Mammalian; Eutheria; Primates; Catarrhini; Hominiidae; Homo.					
TITLE	Bliren, B., Linton, L., Nusbaum, C. and Lander, E.					
JOURNAL	Homo sapiens, clone RP11-619L12					
REFERENCE	2 (bases 1 to 167659)					
AUTHORS	Bliren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barne, N., Bede, F., Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G., Campolano, A., Castle, A., Chepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Dodge, S., Domino, M., Doyle, M., Fenster, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D.,					

Query Match	Local Similarity	96.3%	Score 3690.4	DB 2	Length 167659
Best local	Similarity	99.6%	Pred. No. 0		
Matches 3732	Conservative	0	Mismatches 11	Indels 5	Gaps 3
QY 530	gtggagcttgatgagatgatagtatgctgcatatcgagagctgctcctcagcttgaggatctat	589			
Db 133955	GTGGAGCTTGGCATGATTAATGCAATCGCATATGAGATGTGTCTCAACCTGGATTCAT	134015			
QY 590	accgaccctgagctaaataatcccaaaaggagctgggaggttcgctctctataacaaag	649			
Db 134016	ACCGACCTCGAGCTAAATATCCCAAAAAGAGCTGGAGAGTGGCTGTCTTAATAAAG	134075			
QY 650	agttacataagctgctatcaagtgcgcgctttgttcacgtctgcacatcgagagagatagataa	709			
Db 134076	AGTTACATAGCTGTATCACTGCCCTTTCTTCAGCTGCACATGGAGAGTAAATATAA	134135			
QY 710	cggatgaagcctatcacacattctggaaattctagaatgtctctcctaaagtgttgat	769			
Db 134136	CGGATGAGCTTATACATATTTGGAAAATCTGAAATGTCTCTTAAGTGTGATT	134195			
QY 770	accatattagaaggaggagcattttatgacataaaggagcagctgaacaattctgcctat	829			
Db 134196	ACCATATTAGAGCGGAGCAATTTATGCAATTAAGAGACAGTGCATATTTGCTCAT	134255			
QY 830	agagatbaatlbvclatalatacatgaataatgctctatgaatbctttacbtctca	889			
Db 134256	AGAGTAATATGTGCTATATATCAATGAATATGTCTTAGAATATCTTTATCTTCA	134315			
QY 890	gtttttgagagcctatcacagacactcaattcactctgagttaatttaactctctca	949			
Db 134316	GTTTTGTAGAGCTATATCAGAACCTCAATTAAGTATTAATTAATTCCTCTCA	134375			
QY 950	acttcattcaatcatcatcactcgtctcatctatcattcactagttgttgaagcattcat	1009			
Db 134376	ACTTCATTCAATTCATATCCATCCGTCATTCATTAAGTTGTGAAGTCATTCAAT	134435			
QY 1010	aaatatattacgaatcctttgtctgtgttataaagaatagaacaaaggaatgcctctg	1069			
Db 134436	AAATATTACTGAATTCCTTTGTCTGTGTATATNAATATACAAACAGGAATGCCCTTG	134495			
QY 1070	aggtctcctgcctctttcttgtttgtttcttaactcctgggacataaggagcctcagc	1129			
Db 134496	AGGTTCCTGCCTCTTTTGTGTCTTTTAAATCCCTGGACATAGGGAATACTTCAGC	134555			

[illegible]

QY	2210	atgaagcgtgaattgtgtctctcgcgaataaaactcttggccagcttctcaatc	2269
Db	135633	ATTGACGCTGAATTGTGTGTTCTCTCGCAATGAAATCTTTGGCCAGTGTCATGTCATC	1356922
QY	2270	tgtgaacattatgtagagagagccctaaagagagagccagagtgctctccctatagctgtctc	2329
Db	135653	TGTGACACATTATGAGACAGCCCTAGAGGCCAGAAAGCCAGTGCCTCTTATGCTGCTCT	135752
QY	2330	tccctggcttcgtgacacctctctctctctctgtgttaccttattctttctagttaaaaaac	2389
Db	135753	TCTCGGGCTTCGTGACACCTCTTCTCTCTCTTGTGTACTTTATTTTGTAGTTAAAAAT	135812
QY	2390	tctttttaaggagagaggttctcactctgtcacccagagctggagacagatccaaatcatg	2449
Db	135813	TTTTTTTAGGGAGGGAGGCTCTACCTGTGACCCAGCTGGAGACAGATCAATCATG	1358722
QY	2450	acctaacgtcatgtctctctctctcttggtttcaagtgtaactctgtgtcagaatccctgcag	2509
Db	135873	ACGTACGCTGATGTTCTCTCTCTCTCTTGTTCATGCGCTAATCTGTGTGAGATTCCTGTGAC	1359323
QY	2510	agctcgggttgagacacagatgctgtgtgacacacccgtgcgtgaagagagtttcagaccaatctc	2569
Db	135933	AGCTGGGTGGCACACAGTGTGTGTGACAGCCCTGCTGAAGGAGATTTCAGCCATGAACTTC	1359929
QY	2570	tccagactaaaaaaaccagctctctctctctagctgatagtaatlaaaccaagtgtagctgta	2629
Db	135993	TCCAGACTAAAAATAACCCAGCTCTTCTTACCTGATGAATTAATAACCGGTGACTGTA	1360525
QY	2630	atgctctgaaaggttccatgacatgaaggtttggccgaatagaagcgtgaaacagccccagttta	2689
Db	136053	ATGCTTAAAGGTTCACATGAGAGGTTGGCGATAGAACCTTGAAAGGCCAGCTGTTTA	1361122
QY	2690	gaaatcacccctcgcgaattctgaagccagtgbaacattctcactgtgaaagaaacaagca	2749
Db	136113	GAAATTCACTCTGACTTTTAACTTAAGTCAAGTGAACATTTCTACTGTGAAAGAACAAAGCA	1361722
QY	2750	ggggtttaagagctgtaatccctatctgtgcgcac - tttttttttttaagagagatccag	2808
Db	136173	GGGTTTAGACTGTGAATCTGTAAGGCTGTCATCTTTTTTTTTTAAACAGAGTTCAG	1362322
QY	2809	gtttgtgactataaaccaacatggtacactataatagaaaccaagaccagctcttc	2868
Db	136233	GTTTGTATTATTAACCAACATGTTGTACATTAATTAATGAACACAGACCGGCTTTT	1362922
QY	2869	acgcagcctcagaatctctgtgacgagtagtcagacatctctccaccgagactgaaatg	2928
Db	136293	ACGCACACTCGAATCTTGTGACGAGTAGTCAAGCATCTTCCACCAACTGGAATATG	1363522
QY	2929	aagcgagctgtgtgtgaactcttgatcatcttaagtgtgttggtttaaatctaatctccac	2988
Db	136353	AAGTGCAGTGTGTGGAACCTTGGATCATCTTAAGTTGATTTTGTTTAAATTATGATTCAC	1364122
QY	2989	atatagaaaaaaaccaagatccacataatataaagaaggtttatbgtctcttgaataactcc	3048
Db	136413	ATATGACAAAATAACCGATCCACTTAATTAAATGAGGGTTATGCTATGAAATATCTCC	1364722
QY	3049	tgtgtgttaactctcaataacatctcagtcctaaacagttgtgctccaactcaatgagtctgc	3108
Db	136473	TGTGTGTTTAACTCTATAACATCTTAGTCTTAACAGTGTGGCTTCACTTCAATGAGTGTCC	1365322
QY	3109	tcaaatctcttctcccttaagagatgttctaatcaagaaaaaaatgtaaaatgtag	3168
Db	136533	TCAAACTCTTTTCCTTTAAAGAGATGTTATTATTAACAG - AAAAAAATGTAAATGATAG	1365921
QY	3169	ataataaagagcctctagtggttcttaaaagatgaacatccatctcttaagtaaatgata	3228
Db	136592	ATAATATAAACCTTACTAGTGTCTTTAAAGATGACATCCATATTTCAGTAATATGATA	1366521
QY	3229	attagtcctctctctcttgggaaccttggaaacagatcatctcagatagtggtgtgaaatgc	3288
Db	136652	ATTAGTCTCTCTCTTTGGGCACTTGGAACAGATTCATTTCAATTAAGATGAGGGGTGAATATG	1367111
QY	3289	acatgtaagtgaagcatgtgtgctcagctacgtgaataatgtaaaccttcttctgatt	3348

Db 78623 TTTTATTAAGAGAGGCTCTGACCTGTCACCCAGGCTGAGACACAGATCAATCATG 78564
 QY 2450 actacagcagctgtcag 2509
 Db 78563 ACTACAGCAGCTGTCAG 78504
 QY 2510 agctgagtgagcagcagctgtctctctctctctctctctctctctctctctctc 2569
 Db 78503 AGCTGGGTGACACAGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC 78444
 QY 2570 tccagacataaataaaccagcctctctctctctctctctctctctctctctctct 2629
 Db 78443 TCCAGACTATAAATAACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTA 78384
 QY 2630 atgcttgaagagctcagcagcagctgtctctctctctctctctctctctctctctct 2689
 Db 78383 ATGCTTGAAGAGCT 78324
 QY 2690 gaaatcagcctc 2749
 Db 78323 GAATTCACCT 78264
 QY 2750 ggggttttagacagctgtctctctctctctctctctctctctctctctctct 2808
 Db 78263 GGGGTTTTAGACAGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 78204
 QY 2809 gtttctgattataaaccacacatgtctctctctctctctctctctctctctctct 2868
 Db 78203 GTTCTGATTATAAACCACATGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 78144
 QY 2869 acgacagctcagcagctgtctctctctctctctctctctctctctctctctct 2928
 Db 78143 ACAGACAGCTCAGAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 78084
 QY 2929 aagtcagctgtctgtctgtctgtctgtctgtctgtctgtctgtctgtctgtct 2988
 Db 78083 AAGTCAGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 78024
 QY 2989 atatgcacaaataatccagcagcagcagcagcagcagcagcagcagcagcagc 3048
 Db 78023 ATATGACAAATAATCCAGATCCATTTAAATGAGGTTTATGCTATGAAATATCTC 77964
 QY 3049 tgggggttttaact 3108
 Db 77963 TGGGGTTTAACT 77904
 QY 3109 tcaatccct 3168
 Db 77903 TCAATCCCT 77845
 QY 3169 atataaataatccagcagcagcagcagcagcagcagcagcagcagcagcagc 3228
 Db 77844 ATATAAATAATCCAGATCCATTTAAATGAGGTTTATGCTATGAAATATCTA 77785
 QY 3229 atcagcct 3288
 Db 77784 ATTAGCT 77725
 QY 3289 acctgagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3348
 Db 77724 ACATGATGTAAGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 77665
 QY 3349 ggggggttttagacagctgtctctctctctctctctctctctctctctctct 3408
 Db 77664 GCGGGGTTTTAGACAGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 77605
 QY 3409 cgggttggggggaattctctctctctctctctctctctctctctctctctct 3468
 Db 77604 CCGGTGGGGGAATTCT 77545
 QY 3469 ctgtgataatctgt 3528
 Db 77544 CTGTGATAATCTGT 77485

QY 3529 ggtgaagaaggagctgtacacgacctgtgacatattctctctctctctctctctct 3588
 Db 77484 GGTGAAGAAGGAGCTGTACACGACCTGTGACATTTCTATTCCTGGAAAGGATAT 77425
 QY 3589 tgcagtgctcattctctcagcctcagaataagtgacacctctctctctctctctct 3648
 Db 77424 TGCAGTGCTCATTTCTCAGGCTCAGAAAGTGACACTCTCTGTTCAATTCGACCCCT 77365
 QY 3649 ctcaaccctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3708
 Db 77364 CTCACCCCTCTCAGCAGCTGAGCTCTTTGTGACAGCTGACCTTAATTAATTA 77305
 QY 3709 tgaagaagatgacctataatagtgctgtctgtctgtctgtctgtctgtctgtct 3768
 Db 77304 TGAAGAAGATGACCTATAATATAGTGCTTTTGTGACAGCTGACCTTAATTAATTA 77245
 QY 3769 gaacct 3828
 Db 77244 GAACCT 77185
 QY 3829 aaacacagagagctcagcagcagcagcagcagcagcagcagcagcagcagcag 3888
 Db 77184 AAACACAGAGAGCTCAGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 77125
 QY 3889 aggaagaatgaacacagagagagagagagagagagagagagagagagagagag 3948
 Db 77124 AGGAAGAATGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 77065
 QY 3949 atataagaatcattct 4008
 Db 77064 ATATAAGAATCATTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 77005
 QY 4009 gtttctcccccag 4068
 Db 77004 GTTCTCCCCCAG 76945
 QY 4069 ttgtct 4128
 Db 76944 TTGTCT 76885
 QY 4129 accttttataatgagaagagagagagagagagagagagagagagagagagag 4188
 Db 76884 ACATTTTATAATGAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 76825
 QY 4189 attataatattctcagagagagagagagagagagagagagagagagagagag 4248
 Db 76824 ATTATAATATTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 76765
 QY 4249 accaccacatcagaaaaaataaaaaa 4276
 Db 76764 ACCACCACATCAGAAAAATAAAAA 76737

RESULT 3
 AC093275 180130 bp DNA linear HTG 16-AUG-2001
 LOCUS AC093275
 DEFINITION human sapiens chromosome 5 clone RP11-379A13, WORKING DRAFT
 SEQUENCE 7 unordered pieces.
 AC093275
 AC093275.1 GI:15193409
 VERSION
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 180130)
 AUTHORS DOE Joint Genome Institute.
 TITLE Sequencing of Human Chromosome 5
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 180130)
 AUTHORS DOE Joint Genome Institute.
 TITLE Direct Submission

1910 ggtcaagtgatctctccctccctccagccccagtgagtgaaatcaagcatatacc 1969
OY
17023 ggttcaagtgatctctccctccctccagccccagtgagtgaaatcaagcatatacc 17082
Db
1970 catgccccaaaaatgtttattttatgtgagagcaaggtttacaggtttgttgagcc 2029
OY
17083 catgccccaaaaatgtttattttatgtgagagcaaggtttacaggtttgttgagcc 17142
Db
2030 agttcaaacctccctccctcccaaggatccacccctccctcccaaggtgttgagtt 2089
OY
17143 agtttcaaacctccctccctcccaaggatccacccctccctcccaaggtgttgagtt 17202
Db
2090 acagagcatgagccacccacagctccctccctccctccctccctccctccctccctcc 2149
OY
17203 acagagcatgagccacccacagctccctccctccctccctccctccctccctccctcc 17262
Db
2150 cctgacatcagctccctccctccctccctccctccctccctccctccctccctccctcc 2209
OY
17283 cctgacatcagctccctccctccctccctccctccctccctccctccctccctccctcc 17322
Db
2210 attcaagctgaattgtgtctctccctccctccctccctccctccctccctccctccctcc 2269
OY
17323 attcaagctgaattgtgtctctccctccctccctccctccctccctccctccctccctcc 17382
Db
2270 tctagacatcagctccctccctccctccctccctccctccctccctccctccctccctcc 2329
OY
17383 tctagacatcagctccctccctccctccctccctccctccctccctccctccctccctcc 17442
Db
2330 tctgagacatcagctccctccctccctccctccctccctccctccctccctccctccctcc 2389
OY
17443 tctgagacatcagctccctccctccctccctccctccctccctccctccctccctccctcc 17502
Db
2390 ttttttttgaagggaggtgtcctccctccctccctccctccctccctccctccctccctcc 2449
OY
17503 ttttttttgaagggaggtgtcctccctccctccctccctccctccctccctccctccctcc 17562
Db
2450 actcaagctgaattgtgtctctccctccctccctccctccctccctccctccctccctcc 2509
OY
17563 actcaagctgaattgtgtctctccctccctccctccctccctccctccctccctccctcc 17622
Db
2510 agctggagggagggaggtgtcctccctccctccctccctccctccctccctccctccctcc 2569
OY
17623 agctggagggagggaggtgtcctccctccctccctccctccctccctccctccctccctcc 17682
Db
2570 tccagacatcagctccctccctccctccctccctccctccctccctccctccctccctcc 2629
OY
17683 tccagacatcagctccctccctccctccctccctccctccctccctccctccctccctcc 17742
Db
2630 atgctggaaggtgtcctccctccctccctccctccctccctccctccctccctccctcc 2689
OY
17743 atgctggaaggtgtcctccctccctccctccctccctccctccctccctccctccctcc 17802
Db
2690 gaacatccctccctccctccctccctccctccctccctccctccctccctccctccctcc 2749
OY
17803 gaacatccctccctccctccctccctccctccctccctccctccctccctccctccctcc 17862
Db
2750 aggttttgaagggaggtgtcctccctccctccctccctccctccctccctccctccctcc 2808
OY
17863 aggttttgaagggaggtgtcctccctccctccctccctccctccctccctccctccctcc 17922
Db
2809 gtttttgaagggaggtgtcctccctccctccctccctccctccctccctccctccctccctcc 2868
OY
17923 gtttttgaagggaggtgtcctccctccctccctccctccctccctccctccctccctccctcc 17982
Db
2869 acagagctcagaaatctgtgtgagcagtagtcagagcatcttcaacagcaacttgatgttg 2928
OY
17983 acagagctcagaaatctgtgtgagcagtagtcagagcatcttcaacagcaacttgatgttg 18042
Db
2929 aagtgaggtgtgtgagcagtagtcagagcatcttcaacagcaacttgatgttg 2988
OY
18043 aagtgaggtgtgtgagcagtagtcagagcatcttcaacagcaacttgatgttg 18102
Db

2989 atatgacaaaaatccagatcccaatataaggggtttatgtcatgataatcc 3048
OY
18103 atatgacaaaaatccagatcccaatataaggggtttatgtcatgataatcc 18162
Db
3049 tctgaggttcaatcccaatataaggggtttatgtcatgataatcc 3108
OY
18163 tctgaggttcaatcccaatataaggggtttatgtcatgataatcc 18222
Db
3109 tcaaatcccttccctccctccctccctccctccctccctccctccctccctccctccctcc 3168
OY
18223 tcaaatcccttccctccctccctccctccctccctccctccctccctccctccctccctcc 18281
Db
3169 atataaagagctcagaaatctgtgtgagcagtagtcagagcatcttcaacagcaacttgatgttg 3228
OY
18282 atataaagagctcagaaatctgtgtgagcagtagtcagagcatcttcaacagcaacttgatgttg 18341
Db
3229 atagctcctccctccctccctccctccctccctccctccctccctccctccctccctcc 3288
OY
18342 atagctcctccctccctccctccctccctccctccctccctccctccctccctccctcc 18401
Db
3289 acatgagtgagaaatctgtgtgagcagtagtcagagcatcttcaacagcaacttgatgttg 3348
OY
18402 acatgagtgagaaatctgtgtgagcagtagtcagagcatcttcaacagcaacttgatgttg 18461
Db
3349 gaagtgagaaatctgtgtgagcagtagtcagagcatcttcaacagcaacttgatgttg 3408
OY
18462 gaagtgagaaatctgtgtgagcagtagtcagagcatcttcaacagcaacttgatgttg 18521
Db
3409 ccgtgtgagaaatctgtgtgagcagtagtcagagcatcttcaacagcaacttgatgttg 3468
OY
18522 ccgtgtgagaaatctgtgtgagcagtagtcagagcatcttcaacagcaacttgatgttg 18581
Db
3469 ctgtgagaaatctgtgtgagcagtagtcagagcatcttcaacagcaacttgatgttg 3528
OY
18582 ctgtgagaaatctgtgtgagcagtagtcagagcatcttcaacagcaacttgatgttg 18641
Db
3529 ggtgagaaatctgtgtgagcagtagtcagagcatcttcaacagcaacttgatgttg 3588
OY
18642 ggtgagaaatctgtgtgagcagtagtcagagcatcttcaacagcaacttgatgttg 18701
Db
3589 tgcagtgagaaatctgtgtgagcagtagtcagagcatcttcaacagcaacttgatgttg 3648
OY
18702 tgcagtgagaaatctgtgtgagcagtagtcagagcatcttcaacagcaacttgatgttg 18761
Db
3649 ctcaacatcttcaagcagtagtcagagcatcttcaacagcaacttgatgttg 3708
OY
18762 ctcaacatcttcaagcagtagtcagagcatcttcaacagcaacttgatgttg 18821
Db
3709 tgaagaagaaatctgtgtgagcagtagtcagagcatcttcaacagcaacttgatgttg 3768
OY
18822 tgaagaagaaatctgtgtgagcagtagtcagagcatcttcaacagcaacttgatgttg 18881
Db
3769 gaacatcccttccctccctccctccctccctccctccctccctccctccctccctccctcc 3828
OY
18882 gaacatcccttccctccctccctccctccctccctccctccctccctccctccctccctcc 18941
Db
3829 aaacaaaggggttcaaaatctgtgtgagcagtagtcagagcatcttcaacagcaacttgatgttg 3888
OY
18942 aaacaaaggggttcaaaatctgtgtgagcagtagtcagagcatcttcaacagcaacttgatgttg 19001
Db
3889 agagaaatctgtgtgagcagtagtcagagcatcttcaacagcaacttgatgttg 3948
OY
19002 agagaaatctgtgtgagcagtagtcagagcatcttcaacagcaacttgatgttg 19061
Db
3949 atataaagaaatctgtgtgagcagtagtcagagcatcttcaacagcaacttgatgttg 4008
OY
19062 atataaagaaatctgtgtgagcagtagtcagagcatcttcaacagcaacttgatgttg 19121
Db
4009 gtttttcccaagggaggtgtcctccctccctccctccctccctccctccctccctccctcc 4068
OY
19122 gtttttcccaagggaggtgtcctccctccctccctccctccctccctccctccctccctcc 19181
Db
4069 tttgtctctctccctccctccctccctccctccctccctccctccctccctccctccctcc 4128
OY


```
Db 19182 TTTGCTCTCTCTTTTTCATCCCTTTTAATTTTAAAGCAATGAGGAAAGTGA 19241
Oy 4129 acaatttcaatgaaagagcalttagaacaacaatgacaaagctgagcagc 4188
Db 19242 ACAATTTTAAATGCAAAAGCATGTAGCAAAACAAATGCAATACAAAGCTGACAGC 19301
Oy 4189 attatattaatcttcagggctttagagcctgacacaaattcattccctcaaaagtc 4248
Db 19302 AATTAATTAATTTTCAGGCTTTGAGCTGAACATTAATTCATTATCCCTCAAAAAAGTT 19361
Oy 4249 accaccacacagaaaaaataaaaaa 4276
Db 19362 ACCACCAATCAGAAAAAATAAAAAA 19389

RESULT 4
AC027609/c 157320 bp DNA linear HTG-01-SEP-2000
LOCUS AC027609 34 unordered pieces.
DEFINITION AC027609.3 GI:9958118
ACCESSION AC027609.3 GI:9958118
VERSION HTG: HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eulheria; Primates; Carnivora; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 157320)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 157320)
REFERENCE Waterston,R.H.
AUTHORS Submitted (30-MAR-2000) Genome Sequencing Center, Washington
JOURNAL Direct Submission
AUTHORS University School of Medicine, 4444 Forest Park Parkway, St. Louis,
JOURNAL MO 63108, USA
COMMENT On Sep 1, 2000 this sequence version replaced g1:7637328.
```

```
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH080E21
----- Summary Statistics -----
Sequencing vector: M13; 100%
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 143655 bases at least Q40
Consensus quality: 145934 bases at least Q20
Insert size: 16700; agarose-ftp
Insert size: 153359; sum-of-contigs
Quality coverage: 3.44 in Q20 bases; agarose-ftp
Quality coverage: 3.89 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 34 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 157320: contig of 157320 bp in length
* 1658 157320: gap of unknown length
* 1738 157320: contig of 157320 bp in length
* 3455 157320: gap of unknown length
* 3555 157320: contig of 157320 bp in length
```

```
5137 5235: gap of unknown length
5237 7177: contig of 1941 bp in length
7178 7277: gap of unknown length
7278 8325: contig of 1048 bp in length
8326 8425: gap of unknown length
8426 9445: contig of 1020 bp in length
9446 9546: gap of unknown length
9546 10207: contig of 661 bp in length
10207 10306: gap of unknown length
10306 12221: contig of 1915 bp in length
12221 12322: gap of unknown length
12322 14245: contig of 1924 bp in length
14245 14346: gap of unknown length
14346 16858: contig of 2513 bp in length
16858 16959: gap of unknown length
16959 19404: contig of 2446 bp in length
19404 19505: gap of unknown length
19505 21718: contig of 2214 bp in length
21718 25326: contig of 3408 bp in length
25326 25327: gap of unknown length
25327 28747: contig of 3421 bp in length
28747 32938: gap of unknown length
32938 33039: contig of 4091 bp in length
33039 36347: gap of unknown length
36347 36347: contig of 3209 bp in length
36347 39886: gap of unknown length
39886 39887: contig of 3539 bp in length
39887 43667: gap of unknown length
43667 43766: contig of 3680 bp in length
43766 47542: gap of unknown length
47542 47542: contig of 3776 bp in length
47542 52042: gap of unknown length
52042 52142: contig of 4400 bp in length
52142 55770: gap of unknown length
55770 55770: contig of 3528 bp in length
55770 55771: gap of unknown length
55771 61440: gap of unknown length
61440 61539: contig of 5669 bp in length
61539 65492: gap of unknown length
65492 65492: contig of 3853 bp in length
65492 69190: gap of unknown length
69190 69190: contig of 3698 bp in length
69190 76123: gap of unknown length
76123 76123: contig of 6833 bp in length
76123 82113: gap of unknown length
82113 82113: contig of 5890 bp in length
82113 88806: gap of unknown length
88806 88806: contig of 6593 bp in length
88806 95966: gap of unknown length
95966 95966: contig of 7060 bp in length
95966 102390: gap of unknown length
102390 102390: contig of 6124 bp in length
102390 112332: gap of unknown length
112332 112332: contig of 9942 bp in length
112332 122699: gap of unknown length
122699 122700: contig of 10367 bp in length
122700 129543: gap of unknown length
129543 129543: contig of 6744 bp in length
129543 129644: gap of unknown length
129644 143637: contig of 13993 bp in length
143637 157320: gap of unknown length
157320 157320: contig of 13584 bp in length.

FEATURES
source
1..157320
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="RP11-80E21"
1..1657
/feature="assembly_name:Contig14"
1758..3454
/feature="assembly_name:Contig15"
3555..5136
misc_feature
```

misc_feature /note="assembly_name:Contig17"
5237.7177
/note="assembly_name:Contig18"
7278.8325
/note="assembly_name:Contig19"
8426.9445
/note="assembly_name:Contig20
clone_end:56
vector_side:left"
misc_feature 9346.10206
/note="assembly_name:Contig10"
10307.11221
/note="assembly_name:Contig21"
12322.14245
/note="assembly_name:Contig22"
14346.16858
/note="assembly_name:Contig23"
16959.19404
/note="assembly_name:Contig24"
19505.21718
/note="assembly_name:Contig25"
21819.25226
/note="assembly_name:Contig26"
25327.28747
/note="assembly_name:Contig27"
28848.32938
/note="assembly_name:Contig28"
33039.36247
/note="assembly_name:Contig29"
36348.39886
/note="assembly_name:Contig30"
39987.43666
/note="assembly_name:Contig31"
43767.47542
/note="assembly_name:Contig32"
47643.52042
/note="assembly_name:Contig33"
52143.55670
/note="assembly_name:Contig34"
55771.61439
/note="assembly_name:Contig35"
61540.65392
/note="assembly_name:Contig36"
65493.69190
/note="assembly_name:Contig37"
69291.76123
/note="assembly_name:Contig38"
76224.82113
/note="assembly_name:Contig39"
82214.88806
/note="assembly_name:Contig40"
88907.95966
/note="assembly_name:Contig41"
96067.102190
/note="assembly_name:Contig42"
10291.11232
/note="assembly_name:Contig43"
11233.12269
/note="assembly_name:Contig44"
12800.12943
/note="assembly_name:Contig45"
129644.143636
/note="assembly_name:Contig46"
143737.157320
/note="assembly_name:Contig47"
misc_feature 143737.157320
BASE COUNT 45127 a 32028 c 32232 g 44616 t 3317 others
ORIGIN

Query Match 58.0% Score 2480.4: DB 2: Length 157320:
Best Local Similarity 99.5%: Prid. No. 0:
Matches 2509: Conservative 0: Mismatches 11: Indels 2: Gaps 2:

OY 1756 aagagaaagatcgtctcattcgaacatggggaggaagatctgattgtaaca 1815
|||||
DB 43666 AAGAGAAAAGATCTGTCTATTCAGCATGGGGAGGAGCAAGATTGATTACCA 43607
|||||
OY 1816 tgcctacttctgttctgagatgagctctcctcctcagccagctgagatgacag 1875
|||||
DB 43606 TGCCACTTGTGTGTTGATGAGATGCTCTCCGACACCCAGCCTGAGATGCTG 43547
|||||
OY 1876 tacactcagcctcactcgaactcgaactcgcctccgggttcgaagtatccctgacctgac 1935
|||||
DB 43546 TACACTCAGCTCAGCTCCAGACTCTCGCTCCGGTTCAAGTATCTCTCCCTTAC 43487
|||||
OY 1936 ctccagatgagtggaattcaggaatataccacatgcccagaatgttgattctt 1995
|||||
DB 43486 CTCGGAGTAGTGGAATTACAGGCAATACCAACCAACCAAGTATGTTATTTT 43427
|||||
OY 1996 agtggagacaggttctaacggttctgtaagccagttcacaactcctgacctcaagga 2055
|||||
DB 43426 AGTGAGACAGGGTTCTACCGTGTGTGTCAGCCAGTTCAACCTCTGACCTCAAGGA 43367
|||||
OY 2056 tccacctgcctcaccctcccaagtgctggaattacagcatgagccaccacatgacct 2115
|||||
DB 43366 TCCACCTGCTCACCCTCCCAAGTCTGGATTCAGGCAATGACCCACCATGCT 43307
|||||
OY 2116 ggcctacttctgttcttctgacacataaataatacctacatcctacgtcttctcacc 2175
|||||
DB 43306 GGCCTACTGTGTTTATTCACACATAAATAATACCTACATCAGCTTATTCACAC 43247
|||||
OY 2176 ataagttcagagctgtggaattggtcattggaataatcgaactgaattgttctctctg 2235
|||||
DB 43246 ATTAATTTTCAAGCTGTGGATTTGATTCATTAGAAATTCAGACTAAATTTGTCCTG 43187
|||||
OY 2236 caatgaatctcttgcacagtgctcactcgtcactcgtgacataatgagacagcctagag 2295
|||||
DB 43186 CATATAATCTTTGCCAGTGTTCATGTCACTGTGATGATATATGACACACCTAGAG 43127
|||||
OY 2296 gccagaagccagtgctctcctcattgctcgtcctcctcctggtctctgacactctctc 2355
|||||
DB 43126 GCCAAMACCCAGCTGCTCTCTATTCCTGCTCTCTGCTGCTGCTGCTGCTGCTGCT 43067
|||||
OY 2356 tcccttctcattctcattcttcttctgaataaattcttcttgaagggaggtctccactct 2415
|||||
DB 43066 TCCCTTTTACTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 43007
|||||
OY 2416 gtccacccagagctgagacagacatcgaatcgaatcgaatcgaatcgaatcgaatcgaat 2475
|||||
DB 43006 GTCCACCAAGCTGTGACGACGATTCATCATCTCATCTCATCTCATCTCATCTCTTGG 42947
|||||
OY 2476 ttcacagtaattcttctgacagatctcctgacagctgaggtgagcagctgctgctgac 2535
|||||
DB 42946 TTCATGCTTAATCTGTGTCAGGATTCCTGTGACGCTGCTGCTGCTGCTGCTGCTG 42887
|||||
OY 2536 agctcgtctgaagaggtctcagccatgaaatctcagacataaataaataaataaataaata 2595
|||||
DB 42886 AGCTCGTGTGAAGGAGTTTCACCCATGATCTCTCCAGCTATTAATTAACAGCTCTT 42827
|||||
OY 2596 tctacgtatgaattctaaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaat 2655
|||||
DB 42826 TCTACCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 42767
|||||
OY 2656 tggcgaataagacgctggaacagagccagttcttgaataatcaccctcgaacttctgaactc 2715
|||||
DB 42766 TGCCGATAGAAAGCTGTGAACAGCCAGCTTTAGAAATTCACCTCTGACTTTTAAACCT 42707
|||||
OY 2716 aggtgaacacatctctacgtgaaagacaaagcaggttcttgaactcgtgactcctcctgac 2775
|||||
DB 42706 AGGTGAACCATTTTACTGTGAAGAAACAAAGCAGGTTTATGACTGTGATCTGTATGCT 42647
|||||
OY 2776 tgcacac-ttt 2834
|||||
DB 42646 TGCATCTTTTtt 42587
|||||
OY 2835 acacataataaagaaacacagagcagcttcttctgacagctcgaatctctgctgacga 2894